



5

- 1 -

SEQUENCE LISTING

<110> Ford et al.

<120> EGF MOTIF PROTEIN, EGFL6, MATERIALS AND METHODS

<130> 28110/37665

<140> US 09/981,649

<141> 2001-10-15

<150> US 09/687,860

<151> 2000-10-13

<150> US 09/620,312

<151> 2000-07-19

<150> US 09/363,316

<151> 1999-07-28

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<223> n = A,T,C or G

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<223> Xaa = Any Amino Acid

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Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro	
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gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt	96
Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe	
20 25 30	
cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga	144
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly	
35 40 45	
atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc	192
Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser	
50 55 60	

- 2 -

tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg	240
Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr	
65 70 75 80	

tgt gtg aac tcn agg aca tgt gcc atg ata aac tgt cag tat agc tgt	288
Cys Val Asn Xaa Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys	
85 90 95	

gaa gac aca gaa	300
Glu Asp Thr Glu	
100	

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Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro	
1 5 10 15	

gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt	96
Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe	
20 25 30	

cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga	144
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly	
35 40 45	

atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc	192
Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser	
50 55 60	

tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg	240
Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr	
65 70 75 80	

tgt	gtg	aac	tcn	agg	aca	tgt	gcc	atg	ata	aac	tgt	cag	tat	agc	tgt	288
Cys	Val	Asn	Xaa	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	
				85					90					95		
gaa	gac	aca	gaa	gaa	ggg	cca	cag	tgc	ctg	tgt	cca	tcc	tca	gga	ctc	336
Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	
			100					105					110			
cgc	ctg	gcc	cca	aat	gga	aga	gac	tgt	cta	gat	att	gat	gaa	tgt	gcc	384
Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	
		115					120					125				
tct	ggg	aaa	gtc	atc	tgt	ccc	tac	aat	cga	aga	tgt	gtg	aac	aca	ttt	432
Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	
	130					135					140					
gga	agc	tac	tac	tgc	aaa	tgt	cac	att	ggg	ttc	gaa	ctg	caa	tat	atc	480
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	
145				150					155						160	
agt	gga	cga	tat	gac	tgt	ata	gat	ata	aat	gaa	tgt	act	atg	gat	agc	528
Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser	
				165					170					175		
cat	acg	tgc	agc	cac	cat	gcc	aat	tgc	ttc	aat	acc	caa	ggg	tcc	ttc	576
His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe	
			180					185					190			
aag	tgt	aaa	tgc	aag	cag	gga	tat	aaa	ggc	aat	gga	ctt	cgg	tgt	tct	624
Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser	
		195					200					205				
gct	atc	cct	gaa	aat	tct	gtg	aag	gaa	gtc	ctc	aga	gca	cct	ggg	acc	672
Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr	
	210					215					220					
atc	aaa	gac	aga	atc	aag	aag	ttg	ctt	gct	cac	aaa	aac	agc	atg	aaa	720
Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	His	Lys	Asn	Ser	Met	Lys	
225				230					235						240	
aag	aag	gca	aaa	att	aaa	aat	gtt	acc	cca	gaa	ccc	acc	agg	act	cct	768
Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	Pro	Glu	Pro	Thr	Arg	Thr	Pro	
			245					250						255		
acc	cct	aag	gtg	aac	ttg	cag	ccc	ttc	aac	tat	gaa	gag	ata	gtt	tcc	816
Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser	
			260					265					270			
aga	ggc	ggg	aac	tct	cat	gga	ggg	aaa	aaa	ggg	aat	gaa	gag	aaa	atg	864
Arg	Gly	Gly	Asn	Ser	His	Gly	Gly	Lys	Lys	Gly	Asn	Glu	Glu	Lys	Met	
		275					280					285				
aaa	gag	ggg	ctt	gag	gat	gag	aaa	aga	gaa	gag	aaa	gcc	ctg	aag	aat	912
Lys	Glu	Gly	Leu	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Lys	Ala	Leu	Lys	Asn	
	290					295					300					
gac	ata	gag	gag	cga	agc	ctg	cga	gga	gat	gtg	ttt	ttc	cct	aag	gtg	960
Asp	Ile	Glu	Glu	Arg	Ser	Leu	Arg	Gly	Asp	Val	Phe	Phe	Pro	Lys	Val	
305					310					315					320	

aat gaa gca ggt gaa ttc ggc ctg att ctg gtc caa agg aaa gcg cta 1008
Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu
325 330 335

act tcc aaa ctg gaa cat aaa gat tta aat atc tcg gtt gac tgc agc 1056
Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser
340 345 350

ttc aat cat ggg atc tgt gac tgg aaa cag gat aga gaa gat gat ttt 1104
Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe
355 360 365

gac tgg aat cct gct gat cga gat aat gct att ggc ttc tat atg gca 1152
Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala
370 375 380

gtt ccg gcc ttg gca ggt cac atg aaa gac att ggc cga ttg aaa ctt 1200
Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu
385 390 395 400

ctc cta cct gac ctg caa ccc caa agc aac ttc tgt ttg ctc ttt gat 1248
Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp
405 410 415

tac cgg ctg gcc gga gac aaa gtc ggg aaa ctt cga gtg ttt gtg aaa 1296
Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys
420 425 430

aac agt aac aat gcc ctg gca tgg gag aag acc acg agt gag gat gaa 1344
Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu
435 440 445

aag tgg aag aca ggg aaa att cag ttg tat caa gga act gat gct acc 1392
Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr
450 455 460

aaa agc atc att ttt gaa gca gaa cgt ggc aag ggc aaa acc ggc gaa 1440
Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu
465 470 475 480

atc gca gtg gat ggc gtc ttg ctt gtt tca ggc tta tgt cca gat agc 1488
Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser
485 490 495

ctt tta tct gtg gan nnc tgaatggtac tatctttata tttgactttg 1536
Leu Leu Ser Val Xaa Xaa
500

tatgtcagtt ccctgggtttt tttgatattg catcatagga cctctggcat tttaaaatta 1596
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Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
20 25 30
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
35 40 45

Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
 50 55 60
 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
 65 70 75 80
 Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
 85 90 95
 Glu Asp Thr Glu
 100

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 35 40 45
 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
 50 55 60
 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
 65 70 75 80
 Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
 85 90 95
 Glu Asp Thr Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu
 100 105 110
 Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala
 115 120 125
 Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe
 130 135 140
 Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile
 145 150 155 160
 Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser
 165 170 175
 His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe
 180 185 190
 Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser
 195 200 205
 Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr
 210 215 220
 Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys
 225 230 235 240
 Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro
 245 250 255
 Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser
 260 265 270
 Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met
 275 280 285
 Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn
 290 295 300
 Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val
 305 310 315 320
 Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu
 325 330 335

Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser
 340 345 350
 Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe
 355 360 365
 Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala
 370 375 380
 Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu
 385 390 395 400
 Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp
 405 410 415
 Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys
 420 425 430
 Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu
 435 440 445
 Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr
 450 455 460
 Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu
 465 470 475 480
 Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser
 485 490 495
 Leu Leu Ser Val Asp Asp Xaa Met Val Leu Ser Leu Tyr Leu Thr Leu
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Ile Leu Lys Leu Leu Ala Glu Lys Leu
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 ggaggcggcg gcttagctgc tacgggggtcc ggccggcgcc ctcccagagg gggctcagga 180
 ggaggaagga ggacccgtgc gaga atg cct ctg ccc tgg agc ctt gcg ctc 231
 Met Pro Leu Pro Trp Ser Leu Ala Leu
 1 5
 ccg ctg ctg ctc ccc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt 279
 Pro Leu Leu Leu Pro Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser
 10 15 20 25
 gca agg cat cac ggg ttg tta gca tcg gca cgt cag cct ggg gtc tgt 327
 Ala Arg His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys
 30 35 40
 cac tat gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga aac agc 375
 His Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser
 45 50 55

aag gga gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt ggt gag Lys Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu 60 65 70	423
tgc gtg gga cca aac aaa tgc aga tgc ttt cca gga tac acc ggg aaa Cys Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys 75 80 85	471
acc tgc agt caa gat gtg aat gag tgt gga atg aaa ccc cgg cca tgc Thr Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys 90 95 100 105	519
caa cac aga tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu 110 115 120	567
agt ggc cac atg ctc atg cca gat gct acg tgt gtg aac tct agg aca Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr 125 130 135	615
tgt gcc atg ata aac tgt cag tat agc tgt gaa gac aca gaa gaa ggg Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly 140 145 150	663
cca cag tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca aat gga Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly 155 160 165	711
aga gac tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc atc tgt Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys 170 175 180 185	759
ccc tac aat cga aga tgt gtg aac aca ttt gga agc tac tac tgc aaa Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys 190 195 200	807
tgt cac att ggt ttc gaa ctg caa tat atc agt gga cga tat gac tgt Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys 205 210 215	855
ata gat ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat Ile Asp Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His 220 225 230	903
gcc aat tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc aag cag Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln 235 240 245	951
gga tat aaa ggc aat gga ctt cgg tgt tct gct atc cct gaa aat tct Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser 250 255 260 265	999
gtg aag gaa gtc ctc aga gca cct ggt acc atc aaa gac aga atc aag Val Lys Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys 270 275 280	1047
aag ttg ctt gct cac aaa aac agc atg aaa aag aag gca aaa att aaa Lys Leu Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys 285 290 295	1095

aat gtt acc cca gaa ccc acc agg act cct acc cct aag gtg aac ttg	1143
Asn Val Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu	
300 305 310	
cag ccc ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat	1191
Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His	
315 320 325	
gga ggt aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat	1239
Gly Gly Lys Lys Gly Asn Glu Glu Lys Met Lys Lys Glu Gly Leu Glu Asp	
330 335 340 345	
gag aaa aga gaa gag aaa gcc ctg aag aat gac wta gag gag cga agc	1287
Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn Asp Xaa Glu Glu Arg Ser	
350 355 360	
ctg cga gga gat gtg ttt ttc cct aag gtg aat gaa gca ggt gaa ttc	1335
Leu Arg Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe	
365 370 375	
ggc ctg att ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat	1383
Gly Leu Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His	
380 385 390	
aaa gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt	1431
Lys Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys	
395 400 405	
gac tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct gct gat	1479
Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp	
410 415 420 425	
cga gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt	1527
Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly	
430 435 440	
cac aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa	1575
His Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln	
445 450 455	
ccc caa agc aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc gga gac	1623
Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp	
460 465 470	
aaa gtc ggg aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg	1671
Lys Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu	
475 480 485	
gca tgg gag aag acc acg agt gag gat gaa aag tgg aag aca ggg aaa	1719
Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys	
490 495 500 505	
att cag ttg tat caa gga act gat gct acc aaa agc atc att ttt gaa	1767
Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu	
510 515 520	
gca gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat ggc gtc	1815
Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val	
525 530 535	
ttg ctt gtt tca ggc tta tgt cca gat agc ctt tta tct gtg gat gac	1863
Leu Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp	
540 545 550	

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ccaacagaaa ttattattgt aagatgcctt tmttgtataa gatatgccaa tatttgcttt 2036
aaatatcata tcaactgtatc ttctcagtca tttctgaatc tttccacatt atattataaa 2096
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ctgtttgact cttatgatag tttttggaaa ctatgacatc aaagatagac ttttgcctaa 2276
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<220>

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<222> (357)

<223> Xaa = Any Amino Acid

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Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	Gly	Pro	Asn	Lys	Cys
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Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn
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Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr
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His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro
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Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln
	130					135					140				
Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser
145					150					155					160
Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp
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Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val
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Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu
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Met	Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln
225					230					235					240
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	Leu
			245						250					255	
Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	Arg	Ala
			260					265					270		
Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	His	Lys	Asn
		275					280						285		
Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	Pro	Glu	Pro	Thr
	290					295					300				

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Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu
305          310          315          320
Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu
          325          330          335
Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala
          340          345          350
Leu Lys Asn Asp Xaa Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe
          355          360          365
Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg
          370          375          380
Lys Ala Leu Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val
385          390          395          400
Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu
          405          410          415
Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe
          420          425          430
Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys Asp Ile Gly Arg
          435          440          445
Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu
450          455          460
Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val
465          470          475          480
Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser
          485          490          495
Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr
          500          505          510
Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys
          515          520          525
Thr Gly Glu Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys
530          535          540

Pro Asp Ser Leu Leu Ser Val Asp Asp
545          550

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 Ile Asp Glu Cys Xaa Ser Asn Pro Cys Gln Asn Gly Gly Thr Cys Xaa
 1 5 10 15
 Xaa Xaa Asp Xaa Val Gly Ser Tyr Xaa Cys Xaa Cys Pro Pro Gly Phe
 20 25 30
 Thr Gly Lys Xaa Xaa Xaa Cys Glu Xaa Asn
 35 40

<210> 8
 <211> 39
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 <213> Homo sapiens

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Xaa Asn Glu Cys Thr Met Xaa Xaa Xaa Cys Gln His Xaa Xaa Xaa Cys
 1          5          10          15
Val Asn Thr Xaa Gly Ser Tyr Xaa Cys Lys Cys Xaa Ser Gly Xaa Xaa
 20          25          30
Gly Xaa Xaa Leu Xaa Cys Asp
 35

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 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 9
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 Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr
 20 25 30
 His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro
 35 40 45
 Asp Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
 50 55 60
 Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu
 65 70 75 80
 Arg Leu Ala Pro Asn Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys
 85 90 95
 Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys
 100 105 110
 Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Ile Asn Glu
 115 120 125
 Cys Thr Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn
 130 135 140
 Thr Gln Gly Ser Phe Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly
 145 150 155 160
 Leu Arg Cys Ser

<210> 10
 <211> 45
 <212> PRT
 <213> Homo sapiens

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 Val Xaa Glu Cys Xaa Ser Gly Xaa Gln Xaa Xaa Cys Xaa Ser Ser Xaa
 1 5 10 15
 Xaa Cys Xaa Asn Thr Val Gly Ser Tyr Xaa Cys Arg Cys Arg Pro Gly
 20 25 30
 Trp Xaa Pro Xaa Pro Gly Xaa Pro Asn Xaa Xaa Xaa Asp
 35 40 45

<210> 11
 <211> 58
 <212> PRT
 <213> Mammalian

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<400> 11
 Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
 1 5 10 15
 Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
 20 25 30
 Cys Val Val Gly Tyr Ile Xaa Xaa Xaa Gly Glu Arg Xaa Xaa Cys Gln
 35 40 45
 Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg
 50 55

<210> 12
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Gene-specific PCR primer 10244-52

<400> 12
 ctcacctca agccctctt t

21

<210> 13
 <211> 21
 <212> DNA
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<220>
 <223> Gene-specific PCR primer 10244-51

<400> 13
 ccatgagagt tccgcctct g

21

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<210> 14
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector primer T7

<400> 14
gtaatacgac tcactatagg g                                21

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector primer SP6

<400> 15
atttaggtga cactatagaa gg                                22

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Gene-specific PCR primer 10244-A

<400> 16
cccaggctga cgtgccgatg c                                21

<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Gene-specific PCR primer 10244-B

<400> 17
gcagcaggcc agttagttc c                                21

<210> 18
<211> 502
<212> PRT
<213> Homo sapiens

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<400> 18
Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
1          5          10          15

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Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	20	25	30
Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	35	40	45
Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	50	55	60
Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	65	70	75
Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	85	90	95
Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	100	105	110
Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	115	120	125
Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	130	135	140
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	145	150	155
Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser	165	170	175
His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe	180	185	190
Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser	195	200	205
Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr	210	215	220
Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	His	Lys	Asn	Ser	Met	Lys	225	230	235
Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	Pro	Glu	Pro	Thr	Arg	Thr	Pro	245	250	255
Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser	260	265	270
Arg	Gly	Gly	Asn	Ser	His	Gly	Gly	Lys	Lys	Gly	Asn	Glu	Glu	Lys	Met	275	280	285
Lys	Glu	Gly	Leu	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Lys	Ala	Leu	Lys	Asn	290	295	300
Asp	Ile	Glu	Glu	Arg	Ser	Leu	Arg	Gly	Asp	Val	Phe	Phe	Pro	Lys	Val	305	310	315
Asn	Glu	Ala	Gly	Glu	Phe	Gly	Leu	Ile	Leu	Val	Gln	Arg	Lys	Ala	Leu	325	330	335
Thr	Ser	Lys	Leu	Glu	His	Lys	Asp	Leu	Asn	Ile	Ser	Val	Asp	Cys	Ser	340	345	350
Phe	Asn	His	Gly	Ile	Cys	Asp	Trp	Lys	Gln	Asp	Arg	Glu	Asp	Asp	Phe	355	360	365
Asp	Trp	Asn	Pro	Ala	Asp	Arg	Asp	Asn	Ala	Ile	Gly	Phe	Tyr	Met	Ala	370	375	380
Val	Pro	Ala	Leu	Ala	Gly	His	Met	Lys	Asp	Ile	Gly	Arg	Leu	Lys	Leu	385	390	395
Leu	Leu	Pro	Asp	Leu	Gln	Pro	Gln	Ser	Asn	Phe	Cys	Leu	Leu	Phe	Asp	405	410	415
Tyr	Arg	Leu	Ala	Gly	Asp	Lys	Val	Gly	Lys	Leu	Arg	Val	Phe	Val	Lys	420	425	430
Asn	Ser	Asn	Asn	Ala	Leu	Ala	Trp	Glu	Lys	Thr	Thr	Ser	Glu	Asp	Glu	435	440	445
Lys	Trp	Lys	Thr	Gly	Lys	Ile	Gln	Leu	Tyr	Gln	Gly	Thr	Asp	Ala	Thr	450	455	460
Lys	Ser	Ile	Ile	Phe	Glu	Ala	Glu	Arg	Gly	Lys	Gly	Lys	Thr	Gly	Glu	465	470	475
Ile	Ala	Val	Asp	Gly	Val	Leu	Leu	Val	Ser	Gly	Leu	Cys	Pro	Asp	Ser	485	490	495
Leu	Leu	Ser	Val	Xaa	Xaa											500		

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<210> 19
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<220>
<223> Description of Artificial Sequence: primer

<400> 19
gtcatttctg aatctttcca c 21

<210> 20
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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<400> 20
gaaatgttgc agagagaagc tc 22

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 21
ccagaaccca ccaggactcc 20

<210> 22
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<212> DNA
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<220>
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<400> 22
gggaactgac atacaaagtc 20

<210> 23
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<212> DNA
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ggaggcggcg gcttagctgc tacgggggtcc ggccggcgcc ctcccagggg gggctcagga 180
ggaggaagga ggaccctgac gaga atg cct ctg ccc tgg agc ctt gcg ctc 231
Met Pro Leu Pro Trp Ser Leu Ala Leu
1 5

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ccg ctg ctg ctc tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt	279
Pro Leu Leu Leu Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser	
10 15 20 25	
gca agg cat cac ggg ttg tta gca tcg gca cgt cag cct ggg gtc tgt	327
Ala Arg His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys	
30 35 40	
cac tat gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga aac agc	375
His Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser	
45 50 55	
aag gga gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt ggt gag	423
Lys Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu	
60 65 70	
tgc gtg gga cca aac aaa tgc aga tgc ttt cca gga tac acc ggg aaa	471
Cys Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys	
75 80 85	
acc tgc agt caa gat gtg aat gag tgt gga atg aaa ccc cgg cca tgc	519
Thr Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys	
90 95 100 105	
caa cac aga tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc	567
Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu	
110 115 120	
agt ggc cac atg ctc atg cca gat gct acg tgt gtg aac tct agg aca	615
Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr	
125 130 135	
tgt gcc atg ata aac tgt cag tat agc tgt gaa gac aca gaa gaa ggg	663
Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly	
140 145 150	
cca cag tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca aat gga	711
Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly	
155 160 165	
aga gac tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc atc tgt	759
Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys	
170 175 180 185	
ccc tac aat cga aga tgt gtg aac aca ttt gga agc tac tac tgc aaa	807
Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys	
190 195 200	
tgt cac att ggt ttc gaa ctg caa tat atc agt gga cga tat gac tgt	855
Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys	
205 210 215	
ata gat ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat	903
Ile Asp Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His	
220 225 230	
gcc aat tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc aag cag	951
Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln	
235 240 245	

gga tat aaa ggc aat gga ctt cgg tgt tct gct atc cct gaa aat tct Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser 250 255 260 265	999
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aag ttg ctt gct cac aaa aac agc atg aaa aag aag gca aaa att aaa Lys Leu Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys 285 290 295	1095
aat gtt acc cca gaa ccc acc agg act cct acc cct aag gtg aac ttg Asn Val Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu 300 305 310	1143
cag ccc ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His 315 320 325	1191
gga ggt aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat Gly Gly Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp 330 335 340 345	1239
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ggc ctg att ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat Gly Leu Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His 380 385 390	1383
aaa gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt Lys Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys 395 400 405	1431
gac tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct gct gat Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp 410 415 420 425	1479
cga gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly 430 435 440	1527
cac aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa His Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln 445 450 455	1575
ccc caa agc aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc gga gac Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp 460 465 470	1623
aaa gtc ggg aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg Lys Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu 475 480 485	1671
gca tgg gag aag acc acg agt gag gat gaa aag tgg aag aca ggg aaa Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys 490 495 500 505	1719

att cag ttg tat caa gga act gat gct acc aaa agc atc att ttt gaa 1767
Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu
510 515 520

gca gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat ggc gtc 1815
Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val
525 530 535

ttg ctt gtt tca ggc tta tgt cca gat agc ctt tta tct gtg gat gac 1863
Leu Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp
540 545 550

tgaatgttac tatctttata tttgactttg tatgtcagtt ccctgggtttt tttgatattg 1923

satcatagga cctctggcat tttaaaatta ctaagctgaa aaattgtaat gtaccaacag 1983

aaattattat tgtaagatgc ctttmttgta taagatatgc caatatttgc tttaaatatc 2043

atatcactgt atcttctcag tcatttctga atctttccac attatattat aaaatatgga 2103

aatgtcaggt ttatctcccc tcctcagtat atctgatttg tataagtaag ttgatgagct 2163

tctctctgca acatttctag aaaatagaha aaaaagcaca gagaaatgtt taactgtttg 2223

actcttatga tagttttttg aaactatgac atcaaagata gacttttgcc taagtggctt 2283

agctgggtct ttcatagcca aacttgtata tttaaattct ttgtaataat aatatccaaa 2343

tcatcaaaaa aaaaaaaaaa aa 2365

<210> 24
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<212> PRT
<213> Homo sapiens

<220>
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20 25 30
Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr Lys Leu Ala
35 40 45
Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr
50 55 60
Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys
65 70 75 80
Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn
85 90 95
Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr
100 105 110

His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro
115 120 125

Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln
130 135 140

Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser
145 150 155 160

Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp
165 170 175

Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val
180 185 190

Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu
195 200 205

Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr
210 215 220

Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln
225 230 235 240

Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu
245 250 255

Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala
260 265 270

Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn
275 280 285

Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr
290 295 300

Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu
305 310 315 320

Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu
325 330 335

Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala
340 345 350

Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe
355 360 365

Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg
370 375 380

Lys Ala Leu Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val
385 390 395 400

Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu
405 410 415

Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe
420 425 430

Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys Asp Ile Gly Arg
435 440 445

Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu
 450 455 460

Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val
 465 470 475 480

Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser
 485 490 495

Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr
 500 505 510

Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys
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Thr Gly Glu Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys
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Pro Asp Ser Leu Leu Ser Val Asp Asp
 545 550

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 <211> 22
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 25
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<210> 26
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

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<210> 27
 <211> 2360
 <212> DNA
 <213> Homo sapiens

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 <222> (1) ... (2360)
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ctgctacggg gtccgggccc gcgccctccc gaggggggct caggaggagg aaggaggacc      180
cgtgcgaga      atg cct ctg ccc tgg agc ctt gcg ctc ccg ctg ctg ctc      228
                Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu
                1          5          10

tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt gca agg ggt tct      276
Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg Gly Ser
14          19          24          29

cat cat cat cat cat cac ggg ttg tta gca tgc gca cgt cag cct ggg      324
His His His His His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly
30          35          40          45

gtc tgt cac tat gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga      372
Val Cys His Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg
46          51          56          61

aac agc aag gga gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt      420
Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe
62          67          72          77

ggg gag tgc gtg gga cca aac aaa tgc aga tgc ttt cca gga tac acc      468
Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr
78          83          88          93

ggg aaa acc tgc agt caa gat gtg aat gag tgt gga atg aaa ccc cgg      516
Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg
94          99          104          109

cca tgc caa cac aga tgt gtg aat aca cac gga agc tac aag tgc ttt      564
Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe
110          115          120          125

tgc ctc agt ggc cac atg ctc atg cca gat gct acg tgt gtg aac tct      612
Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser
126          131          136          141

agg aca tgt gcc atg ata aac tgt cag tac agc tgt gaa gac aca gaa      660
Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu
142          147          152          157

gaa ggg cca cag tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca      708
Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro
158          163          168          173

aat gga aga gac tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc      756
Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val
174          179          184          189

atc tgt ccc tac aat cga aga tgt gtg aac aca ttt gga agc tac tac      804
Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr
190          195          200          205

tgc aaa tgt cac att ggt ttc gaa ctg caa tat atc agt gga cga tat      852
Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr
206          211          216          221

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gac tgt ata gat ata aat gaa tgt act atg gat agc cat acg tgc agc Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser 222 227 232 237	900
cac cat gcc aat tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys 238 243 248 253	948
aag cag gga tat aaa ggc aat gga ctt cgg tgt tct gct atc cct gaa Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu 254 259 264 269	996
aat tct gtg aag gaa gtc ctc aga gca cct ggt acc atc aaa gac aga Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg 270 275 280 285	1044
atc aag aag ttg ctt gct cac aaa aac agt atg aaa aag aag gca aaa Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys 286 291 296 301	1092
att aaa aat gtt acc cca gaa ccc acc agg act cct acc cct aag gtg Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val 302 307 312 317	1140
aac ttg cag ccc ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn 318 323 328 333	1188
tct cat gga ggt aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu 334 339 344 349	1236
gag gat gag aaa aga gaa gag aaa gcc ctg aag aat gac ata gag gag Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu 350 355 360 365	1284
cga agc ctg cga gga gat gtg ttt ttc cct aag gtg aat gaa gca ggt Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly 366 371 376 381	1332
gaa ttc ggc ctg att ctg gtc caa agg aaa gcg cta act tcc aaa ctg Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu 382 387 392 397	1380
gaa cat aaa gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly 398 403 408 413	1428
atc tgt gac tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro 414 419 424 429	1476
gct gat cga gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu 430 435 440 445	1524
gca ggt cac aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac Ala Gly His Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp 446 451 456 461	1572
ctg caa ccc caa agc aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala 462 467 472 477	1620

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gga gac aaa gtc ggg aaa ctt cga gtg ttt gtg aaa aac agt aac aat      1668
Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn
478                      483                      488                      493

gcc ctg gca tgg gag aag acc acg agt gag gat gaa aag tgg aag aca      1716
Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr
494                      499                      504                      509

ggg aaa att cag ttg tat caa gga act gat gct acc aaa agc atc att      1764
Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile
510                      515                      520                      525

ttt gaa gca gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat      1812
Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp
526                      531                      536                      541

ggc gtc ttg ctt gtt tca ggc tta tgt cca gat agc ctt tta tct gtg      1860
Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val
542                      547                      552                      557

gat gac tga atgttac tatctttata ttgactttg tatgtcagtt ccttggtttt      1916
Asp Asp *
558

tttgatattg catcatagga cctctggcat tttagaatta ctagctgaaa aattgtaatg      1976

taccaacaga aatattattg taagatgcct ttcttgtata agatatgcca atatttgctt      2036

taaatatcat atcactgtat cttctcagtc atttctgaat cttccacat tatattataa      2096

aatatggaaa tgtcagttta tctccctcc tcagtatatc tgatttgtat aagtaagttg      2156

atgagcttct ctctacaaca tttctagaaa atagaaaaaa aagcacagag aaatgtttaa      2216

ctgtttgact cttatgatac ttcttggaac ctatgacatc aaagatagac ttttgcctaa      2276

gtggcttagc tgggtctttc atagccaaac ttgtatatatt aaattctttg taataataat      2336

atccaaatca tcaaaaaaaaa aaaa                                          2360

<210> 28
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<212> PRT
<213> Homo sapiens

<400> 28
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  20                      25                      30

His His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His
  35                      40                      45

Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys
  50                      55                      60

Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys
  65                      70                      75                      80

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Val	Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	85	90	95
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	Gln	100	105	110
His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	Ser	115	120	125
Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	Cys	130	135	140
Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	Pro	145	150	155
Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	165	170	175
Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	180	185	190
Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	195	200	205
His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	210	215	220
Asp	Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	225	230	235
Asn	Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	245	250	255
Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	260	265	270
Lys	Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	275	280	285
Leu	Leu	Ala	His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	290	295	300
Val	Thr	Pro	Glu	Pro	Thr	Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	305	310	315
Pro	Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser	Arg	Gly	Gly	Asn	Ser	His	Gly	325	330	335
Gly	Lys	Lys	Gly	Asn	Glu	Glu	Lys	Met	Lys	Glu	Gly	Leu	Glu	Asp	Glu	340	345	350
Lys	Arg	Glu	Glu	Lys	Ala	Leu	Lys	Asn	Asp	Ile	Glu	Glu	Arg	Ser	Leu	355	360	365
Arg	Gly	Asp	Val	Phe	Phe	Pro	Lys	Val	Asn	Glu	Ala	Gly	Glu	Phe	Gly	370	375	380
Leu	Ile	Leu	Val	Gln	Arg	Lys	Ala	Leu	Thr	Ser	Lys	Leu	Glu	His	Lys	385	390	395
Asp	Leu	Asn	Ile	Ser	Val	Asp	Cys	Ser	Phe	Asn	His	Gly	Ile	Cys	Asp	405	410	415

Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg
420 425 430

Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His
435 440 445

Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro
450 455 460

Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys
465 470 475 480

Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala
485 490 495

Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile
500 505 510

Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala
515 520 525

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Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp
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<212> DNA
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<222> (190)..(1854)

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ctgctacggg gtccgggccc ggcgcctccc gaggggggct caggaggagg aaggaggacc 180

cgtgcgaga atg cct ctg ccc tgg agc ctt gcg ctc ccg ctg ctg ctc 228
Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu
1 5 10

tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt gca agg cat cat 276
Ser Trp Val Ala Gly Phe Gly Asn Ala Ala Ser Ala Arg His His
14 19 24 29

cac ggg ttg tta gca tcg gca cgt cag cct ggg gtc tgt cac tat gga 324
His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly
30 35 40 45

act	aaa	ctg	gcc	tgc	tgc	tac	ggc	tgg	aga	aga	aac	agc	aag	gga	gtc	372
Thr	Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	
46					51					56					61	
tgt	gaa	gct	aca	tgc	gaa	cct	gga	tgt	aag	ttt	ggg	gag	tgc	gtg	gga	420
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	Gly	
62					67					72					77	
cca	aac	aaa	tgc	aga	tgc	ttt	cca	gga	tac	acc	ggg	aaa	acc	tgc	agt	468
Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	
78					83					88					93	
caa	gat	gtg	aat	gag	tgt	gga	atg	aaa	ccc	cgg	cca	tgc	caa	cac	aga	516
Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	
94					99					104					109	
tgt	gtg	aat	aca	cac	gga	agc	tac	aag	tgc	ttt	tgc	ctc	agt	ggc	cac	564
Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	
110					115					120					125	
atg	ctc	atg	cca	gat	gct	acg	tgt	gtg	aac	tct	agg	aca	tgt	gcc	atg	612
Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	Met	
126					131					136					141	
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Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	
142					147					152					157	
ctg	tgt	cca	tcc	tca	gga	ctc	cgc	ctg	gcc	cca	aat	gga	aga	gac	tgt	708
Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	
158					163					168					173	
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Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	
174					179					184					189	
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Arg	Arg	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	
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Asn	Glu	Cys	Thr	Met	Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	
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Phe	Asn	Thr	Gln	Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	
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ggc	aat	gga	ctt	cgg	tgt	tct	gct	atc	cct	gaa	aat	tct	gtg	aag	gaa	996
Gly	Asn	Gly	Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	
254					259					264					269	
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Val	Leu	Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	
270					275					280					285	
gct	cac	aaa	aac	agt	atg	aaa	aag	aag	gca	aaa	att	aaa	aat	gtt	acc	1092
Ala	His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	
286					291					296					301	

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aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat gag aaa aga Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg 334 339 344 349	1236
gaa gag aaa gcc ctg aag aat gac ata gag gag cga agc ctg cga gga Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg Gly 350 355 360 365	1284
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ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat aaa gat tta Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His Lys Asp Leu 382 387 392 397	1380
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cag gat aga gaa gat gat ttt gac tgg aat cct gct gat cga gat aat Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn 414 419 424 429	1476
gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt cac aag aaa Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys 430 435 440 445	1524
gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa ccc caa agc Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser 446 451 456 461	1572
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aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg gca tgg gag Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu 478 483 488 493	1668
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tat caa gga act gat gct acc aaa agc atc att ttt gaa gca gaa cgt Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg 510 515 520 525	1764
ggc aag ggc aaa acc ggc gaa atc gca gtg gat ggc gtc ttg ctt gtt Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val Leu Leu Val 526 531 536 541	1812
tca ggc tta tgt cca gat agc ctt tta tct gtg gat gac tga atgttac Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp * 542 547 552	1861

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aaaa 2345

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<212> PRT
<213> Homo sapiens

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35 40 45
Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala
50 55 60
Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys
65 70 75 80
Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val
85 90 95
Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn
100 105 110
Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met
115 120 125
Pro Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys
130 135 140
Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro
145 150 155 160
Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile
165 170 175
Asp Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys
180 185 190

Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu
195 200 205

Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys
210 215 220

Thr Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr
225 230 235 240

Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly
245 250 255

Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg
260 265 270

Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys
275 280 285

Asn Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro
290 295 300

Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu
305 310 315 320

Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn
325 330 335

Glu Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys
340 345 350

Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe
355 360 365

Phe Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln
370 375 380

Arg Lys Ala Leu Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser
385 390 395 400

Val Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg
405 410 415

Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly
420 425 430

Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys Asp Ile Gly
435 440 445

Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys
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Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg
465 470 475 480

Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr
485 490 495

Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly
500 505 510

Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly
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Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu
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Leu Leu Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg
15 20 25
cat cac ggg ttg tta gca tcg gca cgt cag cct ggg gtc tgt cac tat 386
His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr
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gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga aac agc aag gga 434
Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly
45 50 55
gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt ggt gag tgc gtg 482
Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val
60 65 70 75
gga cca aac aaa tgc aga tgc ttt cca gga tac acc ggg aaa acc tgc 530
Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys
80 85 90
agt caa gat gtg aat gag tgt gga atg aaa ccc cgg cca tgc caa cac 578
Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His
95 100 105
aga tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc agt ggc 626
Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly
110 115 120
cac atg ctc atg cca gat gct acg tgt gtg aac tct agg aca tgt gcc 674
His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala
125 130 135

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Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln	
140 145 150 155	
tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca aat gga aga gac	770
Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp	
160 165 170	
tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc atc tgt ccc tac	818
Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr	
175 180 185	
aat cga aga tgt gtg aac aca ttt gga agc tac tac tgc aaa tgt cac	866
Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His	
190 195 200	
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Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp	
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ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat gcc aat	962
Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His Ala Asn	
220 225 230 235	
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Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr	
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Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys	
255 260 265	
gaa gtc ctc aga gca cct ggt acc atc aaa gac aga atc aag aag ttg	1106
Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu	
270 275 280	
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Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val	
285 290 295	
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Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro	
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Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly	
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Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys	
335 340 345	
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Arg Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg	
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Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu	
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Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His Lys Ala
380 385 390 395

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400 405 410

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Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg
415 420 425

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Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His
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aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa ccc 1634
Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro
445 450 455

caa agc aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc gga gac aaa 1682
Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys
460 465 470 475

gtc ggg aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg gca 1730
Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala
480 485 490

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Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile
495 500 505

cag ttg tat caa gga act gat gct acc aaa agc atc att ttt gaa gca 1826
Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala
510 515 520

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Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val Leu
525 530 535

ctt gtt tca ggc tta tgt cca gat agc ctt tta tct gtg gat gac tga 1922
Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp
540 545 550 555

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 Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr
 50 55 60
 Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys
 65 70 75 80
 Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn
 85 90 95
 Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr
 100 105 110
 His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro
 115 120 125
 Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln
 130 135 140
 Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser
 145 150 155 160
 Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp
 165 170 175
 Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val
 180 185 190
 Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu
 195 200 205
 Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr
 210 215 220
 Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln
 225 230 235 240
 Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu
 245 250 255
 Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala
 260 265 270
 Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn
 275 280 285
 Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr
 290 295 300

Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	Phe	Asn	Tyr	Glu	Glu	305	310	315	320
Ile	Val	Ser	Arg	Gly	Gly	Asn	Ser	His	Gly	Gly	Lys	Lys	Gly	Asn	Glu	325	330	335	
Glu	Lys	Met	Lys	Glu	Gly	Leu	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Lys	Ala	340	345	350	
Leu	Lys	Asn	Asp	Ile	Glu	Glu	Arg	Ser	Leu	Arg	Gly	Asp	Val	Phe	Phe	355	360	365	
Pro	Lys	Val	Asn	Glu	Ala	Gly	Glu	Phe	Gly	Leu	Ile	Leu	Val	Gln	Arg	370	375	380	
Lys	Ala	Leu	Thr	Ser	Lys	Leu	Glu	His	Lys	Ala	Asp	Leu	Asn	Ile	Ser	385	390	395	400
Val	Asp	Cys	Ser	Phe	Asn	His	Gly	Ile	Cys	Asp	Trp	Lys	Gln	Asp	Arg	405	410	415	
Glu	Asp	Asp	Phe	Asp	Trp	Asn	Pro	Ala	Asp	Arg	Asp	Asn	Ala	Ile	Gly	420	425	430	
Phe	Tyr	Met	Ala	Val	Pro	Ala	Leu	Ala	Gly	His	Lys	Lys	Asp	Ile	Gly	435	440	445	
Arg	Leu	Lys	Leu	Leu	Leu	Pro	Asp	Leu	Gln	Pro	Gln	Ser	Asn	Phe	Cys	450	455	460	
Leu	Leu	Phe	Asp	Tyr	Arg	Leu	Ala	Gly	Asp	Lys	Val	Gly	Lys	Leu	Arg	465	470	475	480
Val	Phe	Val	Lys	Asn	Ser	Asn	Asn	Ala	Leu	Ala	Trp	Glu	Lys	Thr	Thr	485	490	495	
Ser	Glu	Asp	Glu	Lys	Trp	Lys	Thr	Gly	Lys	Ile	Gln	Leu	Tyr	Gln	Gly	500	505	510	
Thr	Asp	Ala	Thr	Lys	Ser	Ile	Ile	Phe	Glu	Ala	Glu	Arg	Gly	Lys	Gly	515	520	525	
Lys	Thr	Gly	Glu	Ile	Ala	Val	Asp	Gly	Val	Leu	Leu	Val	Ser	Gly	Leu	530	535	540	
Cys	Pro	Asp	Ser	Leu	Leu	Ser	Val	Asp	Asp							545	550		